

## SEQUENCE LISTING

<110> Short, Jay M.  
 Kretz, Keith A.  
 Gray, Kevin A.  
 Barton, Nelson Robert  
 Garrett, James B.  
 O' Donoghue, Eileen  
 Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES  
 THEREOF

<130> 09010-029006

<140> US 09/866,379

<141> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

<160> 10

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<211> 1323

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<220>

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<222> (1)...(1320)

<221> misc\_feature

<222> 216

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1				5					10					15		

ccg	caa	tct	gca	ttc	gct	cag	agt	gag	ccg	gag	ctg	aag	ctg	gaa	agt	96
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Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
		35					40					45				
caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	192
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
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aaa	ctg	ggg	tgg	ctg	aca	ccg	cg	ggg	ggg	gag	cta	atc	gcc	tat	ctc	240
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	
65					70					75					80	
gga	cat	tac	caa	cgc	cag	cgt	ctg	gta	gcc	gac	gga	ttg	ctg	gcg	aaa	288
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
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aag	ggc	tgc	ccg	cag	tct	ggg	cag	gtc	gcg	att	att	gct	gat	gtc	gac	336
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
			100					105					110			
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Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
		115					120					125				
gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	
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aac	gtg	act	gac	gcg	atc	ctc	agc	agg	gca	gga	ggg	tca	att	gct	gac	528
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
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ttt	acc	ggg	cat	cgg	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	gtg	ctt	576
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
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aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	gac	gaa	624
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	
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Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
225					230					235					240	
gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768
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Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His			
260	265	270	
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc			864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser			
275	280	285	
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat			912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His			
290	295	300	
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg			960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu			
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ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg			1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu			
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gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt			1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly			
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ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag			1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln			
355	360	365	
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat			1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp			
370	375	380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc			1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr			
385	390	395	400
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca			1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala			
405	410	415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg			1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu			
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Arg Ser His His His His His His			
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&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 2

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Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	35	40	45	
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	50	55	60	
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	65	70	75	80
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	85	90	95	
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	100	105	110	
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	115	120	125	
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	130	135	140	
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	145	150	155	160
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Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	275	280	285	
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His	290	295	300	
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	305	310	315	320
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	325	330	335	
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	340	345	350	
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	355	360	365	
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	370	375	380	
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	385	390	395	400
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	405	410	415	
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	420	425	430	
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49

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33

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 atctgcattc gctcagagtg agccggagct gaagctggaa agtgtggtga ttgtcagtcg 300  
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 ctatctcgga cattaccaac gccagcgtct ggtagccgac ggattgctgg cgaaaaaggg 480  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (188)...(1483)

&lt;221&gt; misc\_feature

&lt;222&gt; 403

&lt;223&gt; n = A,T,C or G

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tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	229
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro	
1 5 10	
tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg	277
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu	
15 20 25 30	
gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	325
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys	
35 40 45	
gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp	
50 55 60	
ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
65 70 75	
tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
80 85 90	
gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat	517
Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
95 100 105 110	
gtc gac gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg	565
Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
115 120 125	
gca cct gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt	613
Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser	
130 135 140	
ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat	661
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
145 150 155	
aac gcg aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att	709
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	

gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
gtg ctt aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag	805
Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln	
195 200 205	
gac gaa agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg	853
Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val	
210 215 220	
agc gcc gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg	901
Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met	
225 230 235	
ctg acg gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg	949
Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro	
240 245 250	
ggg tgg gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt	997
Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser	
255 260 265 270	
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Leu His Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala	
275 280 285	
cgc agc cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg	1093
Arg Ser Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr	
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ccc cat cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca	1141
Pro His Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser	
305 310 315	
gtg ctg ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc	1189
Val Leu Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly	
320 325 330	
gca ctg gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg	1237
Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro	
335 340 345 350	
cca ggt ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac	1285
Pro Gly Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn	
355 360 365	
agc cag tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg	1333
Ser Gln Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met	
370 375 380	
cgt gat aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa	1381
Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys	
385 390 395	
ctg acc ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg	1429



Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser  
 400 405 410

ttg gca ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc 1477  
 Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys  
 415 420 425 430

agt ttg taatgcataa aaaagagcat tcagttacct gaatgctctg aggctgatga 1533  
 Ser Leu

caaacgaaga actgtctaata gcgtagaccg gaaaaggcgt tcacgccgca tccggccact 1593  
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 ccagcaggct ggtgcccaaca gaacgcccc cgaccgcggc atcactcacc gccagcatcg 1833  
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 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
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 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
 85 90 95  
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110  
 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
 115 120 125  
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp  
 130 135 140  
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala  
 145 150 155 160  
 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp  
 165 170 175  
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
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 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu  
 195 200 205  
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
 210 215 220  
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
 225 230 235 240  
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
 245 250 255

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
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 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
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 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His  
                   290                  295                  300  
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305                  310                  315                  320  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
                   325                  330                  335  
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
                   340                  345                  350  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
                   355                  360                  365  
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
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 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
 385                  390                  395                  400  
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
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gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
                   35                  40                  45

caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
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aaa ctg ggt gag ctg aca ccg cgc ggt ggt gag cta atc gcc tat ctc 240  
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
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gga cat tac tgg cgt cag cgt ctg gta gcc gac gga ttg ctg cct aaa 288  
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys

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Cys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp					
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Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro					
115				120				125												
gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432				
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp					
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Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala					
145				150				155				160								
aac	gtg	act	gac	gcg	atc	ctc	gag	agg	gca	gga	ggg	tca	att	gct	gac	528				
Asn	Val	Thr	Asp	Ala	Ile	Leu	Glu	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp					
165				170				175												
ttt	acc	ggg	cat	tat	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	gtg	ctt	576				
Phe	Thr	Gly	His	Tyr	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu					
180				185				190												
aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	gac	gaa	624				
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu					
195				200				205												
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Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala					
210				215				220												
gac	tgt	gtc	tca	tta	acc	ggg	gcg	gta	agc	ctc	gca	tca	atg	ctg	acg	720				
Asp	Cys	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr					
225				230				235				240								
gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768				
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp					
245				250				255												
gga	agg	atc	acc	gat	tca	cac	cag	tgg	aac	acc	ttg	cta	agt	ttg	cat	816				
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His					
260				265				270												
aac	gcg	caa	ttt	gat	ttg	cta	caa	cgc	acg	cca	gag	gtt	gcc	cgc	agc	864				
Asn	Ala	Gln	Phe	Asp	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser					
275				280				285												
cgc	gcc	acc	ccg	tta	tta	gat	ttg	atc	aag	aca	gcg	ttg	acg	ccc	cat	912				
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Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu					
305				310				315				320								

ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg	1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu	
325 330 335	
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Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly	
340 345 350	
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Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln	
355 360 365	
tgg att cag gtt tgc ctg gtc ttc cag act tta cag cag atg cgt gat	1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp	
370 375 380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc	1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr	
385 390 395 400	
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tgc ttg gca	1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala	
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Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu	
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Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys	
85 90 95	
Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp	
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Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro	
115 120 125	
Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp	

130		135		140
Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala				
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Asn Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp				160
	165		170	175
Phe Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu				
	180		185	190
Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu				
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Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala				
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Asp Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr				
225		230		235
Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp				
	245		250	255
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His				
	260		265	270
Asn Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser				
	275		280	285
Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His				
	290		295	300
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu				
305		310		315
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu				
	325		330	335
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly				
	340		345	350
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln				
	355		360	365
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp				
	370		375	380
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr				
385		390		395
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala				
	405		410	415
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu				
	420		425	430